

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/534,593  
Source: PGT/10  
Date Processed by STIC: 5/19/05

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 05/19/2005

PATENT APPLICATION: US/10/534,593

TIME: 10:34:20

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Output Set: N:\CRF4\05182005\J534593.raw

3 <110> APPLICANT: ASHIKARI, MOTOYUKI  
 4 MATSUOKA, MAKOTO  
 5 LIN, SHAOYANG  
 6 YAMAMOTO, TOSHIO  
 7 NISHIMURA, ASUKA  
 8 TAKASHI, TOMONORI  
 10 <120> TITLE OF INVENTION: GENES FOR INCREASING CROP YIELD AND USES THEREOF  
 12 <130> FILE REFERENCE: SHZ-024US  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/534,593  
 C--> 15 <141> CURRENT FILING DATE: 2005-05-11  
 17 <150> PRIOR APPLICATION NUMBER: PCT/JP03/14434  
 18 <151> PRIOR FILING DATE: 2003-11-13  
 20 <150> PRIOR APPLICATION NUMBER: 60/425,919  
 21 <151> PRIOR FILING DATE: 2002-11-13  
 23 <160> NUMBER OF SEQ ID NOS: 14  
 25 <170> SOFTWARE: PatentIn version 3.3  
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 29 <212> TYPE: DNA  
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 60 <220> FEATURE:  
 61 <221> NAME/KEY: Exon

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85 aaattcacac acacactgac acacacaaac cgatcgattg attgattgat a atg aag      177
86                                     Met Lys
87                                     1
89 caa gag cag gtc agg atg gca gtg ctc ctc atg ctc aac tgc ttc gtc      225
90 Gln Glu Gln Val Arg Met Ala Val Leu Leu Met Leu Asn Cys Phe Val
91      5      10      15
93 aag gcc acg gcg ccg ccg cca tgg ccg ccg tcg gct tcg tcc gcc tcc      273
94 Lys Ala Thr Ala Pro Pro Pro Trp Pro Pro Ser Ala Ser Ser Ala Ser
95      20      25      30
97 ttc ctc gac gac ctc ggc gac ctc ggc atc gcg ccg ctc atc cgc gcc      321
98 Phe Leu Asp Asp Leu Gly Asp Leu Gly Ile Ala Pro Leu Ile Arg Ala
99 35      40      45      50
101 gac gag gcg ggc acc gcg cgc gcc tcc gcc gac ttt ggc aac ctc tcc      369
102 Asp Glu Ala Gly Thr Ala Arg Ala Ser Ala Asp Phe Gly Asn Leu Ser
103      55      60      65
105 gtc gcc ggc gtc ggg gcg cct cgg ctc gcc gcc gcc gcc gcc gtc ctc      417
106 Val Ala Gly Val Gly Ala Pro Arg Leu Ala Ala Ala Ala Val Leu
107      70      75      80
109 tac ccg tcg cgc ccc gcc gac atc gcc gcg ctg ctg cgc gcg tcg tgc      465
110 Tyr Pro Ser Arg Pro Ala Asp Ile Ala Ala Leu Leu Arg Ala Ser Cys
111      85      90      95
113 gca cgc ccg gcg ccg ttc gcg gtg tcc gcg cgg ggg tgt ggc cac tcg      513
114 Ala Arg Pro Ala Pro Phe Ala Val Ser Ala Arg Gly Cys Gly His Ser
115      100      105      110
117 gtg cac ggc cag gcc tcc gcg ccc gac ggc gtc gtc gtc gac atg gcg      561
118 Val His Gly Gln Ala Ser Ala Pro Asp Gly Val Val Val Asp Met Ala
119 115      120      125      130
121 tcg ctc ggc cgc ctg cag ggc ggc ggc gcg cgg cgc ctc gcc gtg tca      609
122 Ser Leu Gly Arg Leu Gln Gly Gly Gly Ala Arg Arg Leu Ala Val Ser
123      135      140      145
125 gtg gag ggg cgg tac gtc gac gcc ggc ggc gag cag ctg tgg gtg gac      657
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131      165      170      175
133 gac tac ctc cac ctc acc gtc ggc ggc acg ctg tcc aac gcc ggc atc      753
134 Asp Tyr Leu His Leu Thr Val Gly Gly Thr Leu Ser Asn Ala Gly Ile
135      180      185      190
137 agc ggc cag gcc ttc cgc cat ggc ccc cag att tcc aac gtg cta gag      801
138 Ser Gly Gln Ala Phe Arg His Gly Pro Gln Ile Ser Asn Val Leu Glu
139 195      200      205      210
141 ctc gac gtc atc acc ggtacgtaga tccatcacat ctactaagac acgcgccgcc      856
142 Leu Asp Val Ile Thr
143      215
145 atgatcgagg taattaaggt ataggtgttt tgacgtatac atgtatctgc a ggt gtc      913
146      Gly Val
149 ggg gag atg gtg acg tgc tcg aag gag aag gcg ccg gac ctg ttc gac      961
150 Gly Glu Met Val Thr Cys Ser Lys Glu Lys Ala Pro Asp Leu Phe Asp
151      220      225      230
153 gcg gtg ctg ggc ggc ctg ggc cag ttc ggc gtc atc acg cgg gcg cgc      1009
154 Ala Val Leu Gly Gly Leu Gly Gln Phe Gly Val Ile Thr Arg Ala Arg
155      235      240      245
157 atc ccg ctc gcg ccg gcg ccg gcg agg gcg cgg tgg gtg cgg ttc gtg      1057
158 Ile Pro Leu Ala Pro Ala Pro Ala Arg Ala Arg Trp Val Arg Phe Val
159 250      255      260      265
161 tac acg acg gcg gcg gcg atg acg gcc gac cag gag cgc ctc atc gcc      1105
162 Tyr Thr Thr Ala Ala Ala Met Thr Ala Asp Gln Glu Arg Leu Ile Ala
163      270      275      280
165 gtc gat cgc gcc ggc ggc gcc ggc gcg gtg ggc ggg ctg atg gac tac      1153
166 Val Asp Arg Ala Gly Gly Ala Gly Ala Val Gly Gly Leu Met Asp Tyr
167      285      290      295
169 gtc gag ggc tcg gtc cac ctg aac cag ggc ctg gtc gag acc tgg cgc      1201
170 Val Glu Gly Ser Val His Leu Asn Gln Gly Leu Val Glu Thr Trp Arg
171      300      305      310
173 acg cag ccg cag ccg cct tcg ccg tcc tcc tcc tcc tcc tca tcc ttc      1249
174 Thr Gln Pro Gln Pro Pro Ser Pro Ser Ser Ser Ser Ser Ser Ser Phe
175      315      320      325
177 ttc tcc gac gcc gac gag gcc cgc gtc gcc gcg ctc gcc aag gag gcc      1297
178 Phe Ser Asp Ala Asp Glu Ala Arg Val Ala Ala Leu Ala Lys Glu Ala
179 330      335      340      345
181 ggc ggc gtg ctg tat ttc ctc gag ggc gcc atc tac ttc ggc ggc gcc      1345
182 Gly Gly Val Leu Tyr Phe Leu Glu Gly Ala Ile Tyr Phe Gly Gly Ala
183      350      355      360
185 gcc ggg ccg tcc gcc gcc gac gtt gac aag gtatactagc tagctactag      1395
186 Ala Gly Pro Ser Ala Ala Asp Val Asp Lys
187      365      370
189 cttgctctgc gctgagccga ccagagcggg tcccacctcg tgatgatggc gggaacaact      1455
191 aagctgcaaa aacttttggc gccacctggg gcttacgctt acgcacgcat gcaattaagg      1515
193 ggtgttctag atggggctaa aacttttttag cccatgtcac atcggtatgtt tggacgctaa      1575
195 tttggagtat taaatataga ctaataaaaa aactaatttc ataaatgaga gctaattccgc      1635
197 gagacgaatt ttttaagcct aattaatcta taattataaa agttttattgt agcatcacat      1695

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203 gtgacatgga cttggaataa gtccgtggaa accaaacaga ccctaacggt gcatgaaatt 1875
205 gaagtctctt gcgccgtcga catcgtcgta cttggcctac cacttttgtc tgccacgcga 1935
207 tgcacctctc gctatcacac acctaactgg aagtaattaa ataattattc gattctgtgt 1995
209 taattttttt ttatcttcct tagttcccgg agagacaaaag attagatact atagtagcaa 2055
211 cttagtaagc tagtatatgg agtattaggt tagtcgtctc cactaagctt aaacaggtgt 2115
213 ataaaaatata tgcacgtctc gatcgtgaca tattctttta gctacttatg gtgaaaactt 2175
215 tttcgtccaa aacagtga aaacgtgcgtg ctagtgtagg tagtagctac caggacgaat 2235
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219 cagtcttcag aacgcacaac ttaaacaggt atttttgtat tatatttttt taaaaaaaaa 2355
221 taaaggtaat aaaattatgg tattgtaaaa gtatattttt aaggaaaatc atataacca 2415
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259 ttgcaacacg accgaccaac tatgttggct ctatatagat agctagctag ttattccatg 3555
261 catatacagt ttgcatttcc tagctatagc ttttgctatg tgatccgaga agatcctgca 3615
263 tgccacacg tgacacgtca cacacaaagt tggacaaagt actgcctcac tttatccttg 3675
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267 gatcaaattt cggatgatctc tctgcaaaga atttgatgaa ttttaccac atatatgctt 3795
269 taattttctt gcttgatttt atttgcag agg atg gat gtg ctg cgt cgc gag 3847
270 Arg Met Asp Val Leu Arg Arg Glu
271 375
273 ctg cgg cac gag cgc ggg ttc gtg ttc gcg cag gac gtg gcg tac gcc 3895
274 Leu Arg His Glu Arg Gly Phe Val Phe Ala Gln Asp Val Ala Tyr Ala
275 380 385 390 395
277 ggg ttc ctg gac cgc gtc cac gac ggc gag ctc aag ctc cgc gcc gcg 3943
278 Gly Phe Leu Asp Arg Val His Asp Gly Glu Leu Lys Leu Arg Ala Ala
279 400 405 410
281 ggg ctc tgg gac gtg ccg cac cca tgg ctg aac ctg ttc ctc ccc cgc 3991
282 Gly Leu Trp Asp Val Pro His Pro Trp Leu Asn Leu Phe Leu Pro Arg
283 415 420 425
285 tcc ggc gtc ctc gcc ttc gcc gac ggc gtc ttc cac ggc atc ctc agc 4039
286 Ser Gly Val Leu Ala Phe Ala Asp Gly Val Phe His Gly Ile Leu Ser

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291          445          450          455
293 aag taataataat aataaaaagc ttactacat atacacatgt atataatttt      4140
294 Lys
295 460
297 tacgggggtgg attttttcgt tcaaaatgac gaccctcat attgtgctg tcgtctgaaa      4200
299 acttattaaa atgtttaaat aaaaaattaa tatgatacat aaatatatta tatatcacta      4260
301 tataaacatt gtaatcttaa actcaacttg cacaagtagt aaaaaaacia atttgactgc      4320
303 aaatagtggt tactaagtta tttatttact tatgctagta tgctacttga atttaaactgc      4380
305 acatatttat gaagtggat attatatatt tccagagtat ttttatgggt cttttacgac      4440
307 atgaaaaaca atgtccgttc tcttgaagga tgaatagact ttccttaatt ttaacatata      4500
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310                                     Trp Asp Ser Asn Met
311                                     465
313 tcg gca gtg atc acc gac gac gac ggt gac gag gtg ttc tac acg gtg      4604
314 Ser Ala Val Ile Thr Asp Asp Asp Gly Asp Glu Val Phe Tyr Thr Val
315          470          475          480
317 ggg atc ctg cgg tcg gcg gcg gcg gcc ggc gac gtg ggg agg ctg gag      4652
318 Gly Ile Leu Arg Ser Ala Ala Ala Ala Gly Asp Val Gly Arg Leu Glu
319          485          490          495
321 gag cag aac gac gag atc ttg ggt ttc tgc gag gtg gcc ggg ata gcc      4700
322 Glu Gln Asn Asp Glu Ile Leu Gly Phe Cys Glu Val Ala Gly Ile Ala
323          500          505          510
325 tac aag cag tac ctg cct tac tac ggc agc cag gca gag tgg cag aag      4748
326 Tyr Lys Gln Tyr Leu Pro Tyr Tyr Gly Ser Gln Ala Glu Trp Gln Lys
327          515          520          525
329 cgg cac ttc ggt gcc aat ctc tgg cca aga ttc gtg cag cgg aag agc      4796
330 Arg His Phe Gly Ala Asn Leu Trp Pro Arg Phe Val Gln Arg Lys Ser
331 530          535          540          545
333 aag tat gat cca aag gcc atc ctg tcc cgt ggc cag ggg att ttc acg      4844
334 Lys Tyr Asp Pro Lys Ala Ile Leu Ser Arg Gly Gln Gly Ile Phe Thr
335          550          555          560
337 tca cca ctc gca tgaaatgaca catgtatgca aatgcatatc tacatgcgta      4896
338 Ser Pro Leu Ala
339          565
341 tatatacacg tatatatacg tatgtatgca tacacatatg ggtgtactgt gcatacgtaa      4956
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345 aagctaatat aaataatgga gtagtagtat atatgtagtg cgagataatt aagtagtggt      5076
347 tttgcctact aaaaggagag gcaaagtagt actgtgatgc atgcatgcca actaatagggt      5136
349 gataagtacg tgtgtgtggc cgcattgatg attagaagaa gtgtgttttt aattaattaa      5196
351 ttaggtcatg tatgtaaata tatagtacag tactacgtac tactagtgtg ctaccagcca      5256
353 atttgcattg atgcatggat gccttcatat gcatgtcgat ctcaaagcta cggcatgctt      5316
355 gaatgcatca tgatgcatat ctatcgtcgt cttgtgggtg taaactaaat taatcttagt      5376
357 tatatgtatt ataagtttgc aata      5400
360 <210> SEQ ID NO: 2
361 <211> LENGTH: 2302
362 <212> TYPE: DNA

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:4; N Pos. 4049,4050,4051,4052,4053,4054,4055,4056,4057,4058,4059,4060

Seq#:4; N Pos. 4061,4062

**VERIFICATION SUMMARY**

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L:14 M:270 C: Current Application Number differs, Replaced Application Number

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:861 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:4021